

SEQUENCE LISTING

<110> POWDERJECT RESEARCH LIMITED AND GLAXO GROUP LIMITED

<120> ADJUVANT

<130> N.88232 GCW

<160> 12

<170> PatentIn version 3.1

<210> 1

<211> 12

<212> PRT

<213> Artificial sequence

<220>

<223> HBsAg in BLAB/C mice

<400> 1

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<210> 2

<211> 9

<212> PRT

<213> Artificial sequence

<220>

<223> HSV CD8 in BLAB/C mice

<400> 2

His Gly Pro Ser Leu Tyr Arg Thr Phe

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<210> 3

<211> 1503

<212> DNA

<213> Artificial sequence

<220>

<223> nucleotide sequence of p55 gag insert in pGagOptrpr2

<400> 3

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<210> 4

<211> 500

<212> PRT

<213> Artificial sequence

<220>

<223> amino acid sequence of p55 gag insert in pGagOptrpr2

<400> 4

Met Gly Ala Arg Ala Ser Val Leu Ser Gly Gly Glu Leu Asp Arg Trp
1 5 10 15

Glu Lys Ile Arg Leu Arg Pro Gly Gly Lys Lys Lys Tyr Lys Leu Lys
20 25 30

His Ile Val Trp Ala Ser Arg Glu Leu Glu Arg Phe Ala Val Asn Pro
35 40 45

Gly Leu Leu Glu Thr Ser Glu Gly Cys Arg Gln Ile Leu Gly Gln Leu
50 55 60

Gln Pro Ser Leu Gln Thr Gly Ser Glu Glu Leu Arg Ser Leu Tyr Asn
65 70 75 80

Thr Val Ala Thr Leu Tyr Cys Val His Gln Arg Ile Glu Ile Lys Asp
85 90 95

Thr Lys Glu Ala Leu Asp Lys Ile Glu Glu Glu Gln Asn Lys Ser Lys
100 105 110

Lys Lys Ala Gln Gln Ala Ala Ala Asp Thr Gly His Ser Asn Gln Val
115 120 125

Ser Gln Asn Tyr Pro Ile Val Gln Asn Ile Gln Gly Gln Met Val His
130 135 140

Gln Ala Ile Ser Pro Arg Thr Leu Asn Ala Trp Val Lys Val Val Glu
 145 150 155 160

Glu Lys Ala Phe Ser Pro Glu Val Ile Pro Met Phe Ser Ala Leu Ser
 165 170 175

Glu Gly Ala Thr Pro Gln Asp Leu Asn Thr Met Leu Asn Thr Val Gly
 180 185 190

Gly His Gln Ala Ala Met Gln Met Leu Lys Glu Thr Ile Asn Glu Glu
 195 200 205

Ala Ala Glu Trp Asp Arg Val His Pro Val His Ala Gly Pro Ile Ala
 210 215 220

Pro Gly Gln Met Arg Glu Pro Arg Gly Ser Asp Ile Ala Gly Thr Thr
 225 230 235 240

Ser Thr Leu Gln Glu Gln Ile Gly Trp Met Thr Asn Asn Pro Pro Ile
 245 250 255

Pro Val Gly Glu Ile Tyr Lys Arg Trp Ile Ile Leu Gly Leu Asn Lys
 260 265 270

Ile Val Arg Met Tyr Ser Pro Thr Ser Ile Leu Asp Ile Arg Gln Gly
 275 280 285

Pro Lys Glu Pro Phe Arg Asp Tyr Val Asp Arg Phe Tyr Lys Thr Leu
 290 295 300

Arg Ala Glu Gln Ala Ser Gln Glu Val Lys Asn Trp Met Thr Glu Thr
 305 310 315 320

Leu Leu Val Gln Asn Ala Asn Pro Asp Cys Lys Thr Ile Leu Lys Ala
 325 330 335

Leu Gly Pro Ala Ala Thr Leu Glu Glu Met Met Thr Ala Cys Gln Gly
 340 345 350

Val Gly Gly Pro Gly His Lys Ala Arg Val Leu Ala Glu Ala Met Ser
 355 360 365

Gln Val Thr Asn Ser Ala Thr Ile Met Met Gln Arg Gly Asn Phe Arg
 370 375 380

Asn Gln Arg Lys Ile Val Lys Cys Phe Asn Cys Gly Lys Glu Gly His
385 390 395 400

Thr Ala Arg Asn Cys Arg Ala Pro Arg Lys Lys Gly Cys Trp Lys Cys
405 410 415

Gly Lys Glu Gly His Gln Met Lys Asp Cys Thr Glu Arg Gln Ala Asn
420 425 430

Phe Leu Gly Lys Ile Trp Pro Ser Tyr Lys Gly Arg Pro Gly Asn Phe
435 440 445

Leu Gln Ser Arg Pro Glu Pro Thr Ala Pro Pro Glu Glu Ser Phe Arg
450 455 460

Ser Gly Val Glu Thr Thr Thr Pro Pro Gln Lys Gln Glu Pro Ile Asp
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Pro Ser Ser Gln
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<210> 5

<211> 1515

<212> DNA

<213> Artificial sequence

<220>

<223> nucleotide sequence of the p17/24trNEF insert in p17/24trNEF1

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ctagaacgat tcgcagttaa tcttggcctg ttagaaacat cagaaggctg tagacaaata	180
ctgggacagc tacaaccatc ccttcagaca ggatcagaag aacttagatc attatataat	240
acagtagcaa ccctctattg tgtgcatcaa aggatagaga taaaagacac caaggaagct	300
ttagacaaga tagaggaaga gcaaaacaaa agtaagaaaa aagcacagca agcagcagct	360
gacacaggac acagcaatca ggtcagccaa aattacccta tagtgcagaa catccagggg	420

caaatggtac atcaggccat atcacctaga actttaaatg catgggtaaa agtagtagaa 480
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 ccacaagatt taaacaccat gctaaacaca gtggggggac atcaagcagc catgcaaag 600
 ttaaaagaga ccatcaatga ggaagctgca gaatgggata gaggatcatcc agtgcatgca 660
 gggcctattg caccaggcca gatgagagaa ccaaggggaa gtgacatagc aggaactact 720
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<210> 6

<211> 504

<212> PRT

<213> Artificial sequence

<220>

<223> amino acid sequence of the p17/24trNEF insert in p17/24trNEF1

<400> 6

Met Gly Ala Arg Ala Ser Val Leu Ser Gly Gly Glu Leu Asp Arg Trp
 1 5 10 15

Glu Lys Ile Arg Leu Arg Pro Gly Gly Lys Lys Lys Tyr Lys Leu Lys
 20 25 30

His Ile Val Trp Ala Ser Arg Glu Leu Glu Arg Phe Ala Val Asn Pro
 35 40 45

Gly Leu Leu Glu Thr Ser Glu Gly Cys Arg Gln Ile Leu Gly Gln Leu
 50 55 60

Gln Pro Ser Leu Gln Thr Gly Ser Glu Glu Leu Arg Ser Leu Tyr Asn
 65 70 75 80

Thr Val Ala Thr Leu Tyr Cys Val His Gln Arg Ile Glu Ile Lys Asp
 85 90 95

Thr Lys Glu Ala Leu Asp Lys Ile Glu Glu Glu Gln Asn Lys Ser Lys
 100 105 110

Lys Lys Ala Gln Gln Ala Ala Ala Asp Thr Gly His Ser Asn Gln Val
 115 120 125

Ser Gln Asn Tyr Pro Ile Val Gln Asn Ile Gln Gly Gln Met Val His
 130 135 140

Gln Ala Ile Ser Pro Arg Thr Leu Asn Ala Trp Val Lys Val Val Glu
 145 150 155 160

Glu Lys Ala Phe Ser Pro Glu Val Ile Pro Met Phe Ser Ala Leu Ser
 165 170 175

Glu Gly Ala Thr Pro Gln Asp Leu Asn Thr Met Leu Asn Thr Val Gly
 180 185 190

Gly His Gln Ala Ala Met Gln Met Leu Lys Glu Thr Ile Asn Glu Glu
 195 200 205

Ala Ala Glu Trp Asp Arg Val His Pro Val His Ala Gly Pro Ile Ala
 210 215 220

Pro Gly Gln Met Arg Glu Pro Arg Gly Ser Asp Ile Ala Gly Thr Thr
 225 230 235 240

Ser Thr Leu Gln Glu Gln Ile Gly Trp Met Thr Asn Asn Pro Pro Ile
 245 250 255

Pro Val Gly Glu Ile Tyr Lys Arg Trp Ile Ile Leu Gly Leu Asn Lys
 260 265 270

Ile Val Arg Met Tyr Ser Pro Thr Ser Ile Leu Asp Ile Arg Gln Gly
 275 280 285
 Pro Lys Glu Pro Phe Arg Asp Tyr Val Asp Arg Phe Tyr Lys Thr Leu
 290 295 300
 Arg Ala Glu Gln Ala Ser Gln Glu Val Lys Asn Trp Met Thr Glu Thr
 305 310 315 320
 Leu Leu Val Gln Asn Ala Asn Pro Asp Cys Lys Thr Ile Leu Lys Ala
 325 330 335
 Leu Gly Pro Ala Ala Thr Leu Glu Glu Met Met Thr Ala Cys Gln Gly
 340 345 350
 Val Gly Gly Pro Gly His Lys Ala Arg Val Leu Val Gly Phe Pro Val
 355 360 365
 Thr Pro Gln Val Pro Leu Arg Pro Met Thr Tyr Lys Ala Ala Val Asp
 370 375 380
 Leu Ser His Phe Leu Lys Glu Lys Gly Gly Leu Glu Gly Leu Ile His
 385 390 395 400
 Ser Gln Arg Arg Gln Asp Ile Leu Asp Leu Trp Ile Tyr His Thr Gln
 405 410 415
 Gly Tyr Phe Pro Asp Trp Gln Asn Tyr Thr Pro Gly Pro Gly Val Arg
 420 425 430
 Tyr Pro Leu Thr Phe Gly Trp Cys Tyr Lys Leu Val Pro Val Glu Pro
 435 440 445
 Asp Lys Val Glu Glu Ala Asn Lys Gly Glu Asn Thr Ser Leu Leu His
 450 455 460
 Pro Val Ser Leu His Gly Met Asp Asp Pro Glu Arg Glu Val Leu Glu
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 Trp Arg Phe Asp Ser His Leu Ala Phe His His Val Ala Arg Glu Leu
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 His Pro Glu Tyr Phe Lys Asn Cys
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<210> 7

<211> 1518

<212> DNA

<213> Artificial sequence

<220>

<223> nucleotide sequence of the p17/24opt/trNef insert in p17/24opt/trNef1

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agagtgttga tggtgggttt tccagtcaca cctcagggtac ctttaagacc aatgacttac     1140
aaggcagctg tagatcttag ccacttttta aaagaaaagg ggggactgga agggctaatt     1200
caactccaaa gaagacaaga tctccttgat ctgtggatct accacacaca aggctacttc     1260
cctgattggc agaactacac accaggggcca ggggtcagat atccactgac ctttggatgg     1320
tgctacaagc tagtaccagt tgagccagat aaggtagaag aggccaataa aggagagaac     1380
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<210> 8

<211> 505

<212> PRT

<213> Artificial sequence

<220>

<223> amino acid sequence of the p17/24opt/trNef insert in p17/24opt/trNef1

<400> 8

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Glu Lys Ile Arg Leu Arg Pro Gly Gly Lys Lys Lys Tyr Lys Leu Lys
 20 25 30

His Ile Val Trp Ala Ser Arg Glu Leu Glu Arg Phe Ala Val Asn Pro
 35 40 45

Gly Leu Leu Glu Thr Ser Glu Gly Cys Arg Gln Ile Leu Gly Gln Leu
 50 55 60

Gln Pro Ser Leu Gln Thr Gly Ser Glu Glu Leu Arg Ser Leu Tyr Asn
 65 70 75 80

Thr Val Ala Thr Leu Tyr Cys Val His Gln Arg Ile Glu Ile Lys Asp
 85 90 95

Thr Lys Glu Ala Leu Asp Lys Ile Glu Glu Glu Gln Asn Lys Ser Lys
 100 105 110

Lys Lys Ala Gln Gln Ala Ala Ala Asp Thr Gly His Ser Asn Gln Val
 115 120 125

Ser Gln Asn Tyr Pro Ile Val Gln Asn Ile Gln Gly Gln Met Val His
 130 135 140

Gln Ala Ile Ser Pro Arg Thr Leu Asn Ala Trp Val Lys Val Val Glu
 145 150 155 160

Glu Lys Ala Phe Ser Pro Glu Val Ile Pro Met Phe Ser Ala Leu Ser
 165 170 175

Glu Gly Ala Thr Pro Gln Asp Leu Asn Thr Met Leu Asn Thr Val Gly
 180 185 190

Gly His Gln Ala Ala Met Gln Met Leu Lys Glu Thr Ile Asn Glu Glu
 195 200 205

Ala Ala Glu Trp Asp Arg Val His Pro Val His Ala Gly Pro Ile Ala
 210 215 220

Pro Gly Gln Met Arg Glu Pro Arg Gly Ser Asp Ile Ala Gly Thr Thr
 225 230 235 240

Ser Thr Leu Gln Glu Gln Ile Gly Trp Met Thr Asn Asn Pro Pro Ile
 245 250 255

Pro Val Gly Glu Ile Tyr Lys Arg Trp Ile Ile Leu Gly Leu Asn Lys
 260 265 270

Ile Val Arg Met Tyr Ser Pro Thr Ser Ile Leu Asp Ile Arg Gln Gly
 275 280 285

Pro Lys Glu Pro Phe Arg Asp Tyr Val Asp Arg Phe Tyr Lys Thr Leu
 290 295 300

Arg Ala Glu Gln Ala Ser Gln Glu Val Lys Asn Trp Met Thr Glu Thr
 305 310 315 320

Leu Leu Val Gln Asn Ala Asn Pro Asp Cys Lys Thr Ile Leu Lys Ala
 325 330 335

Leu Gly Pro Ala Ala Thr Leu Glu Glu Met Met Thr Ala Cys Gln Gly
 340 345 350

Val Gly Gly Pro Gly His Lys Ala Arg Val Leu Met Val Gly Phe Pro
 355 360 365

Val Thr Pro Gln Val Pro Leu Arg Pro Met Thr Tyr Lys Ala Ala Val
 370 375 380

Asp Leu Ser His Phe Leu Lys Glu Lys Gly Gly Leu Glu Gly Leu Ile

385

390

395

400

His Ser Gln Arg Arg Gln Asp Ile Leu Asp Leu Trp Ile Tyr His Thr
 405 410 415

Gln Gly Tyr Phe Pro Asp Trp Gln Asn Tyr Thr Pro Gly Pro Gly Val
 420 425 430

Arg Tyr Pro Leu Thr Phe Gly Trp Cys Tyr Lys Leu Val Pro Val Glu
 435 440 445

Pro Asp Lys Val Glu Glu Ala Asn Lys Gly Glu Asn Thr Ser Leu Leu
 450 455 460

His Pro Val Ser Leu His Gly Met Asp Asp Pro Glu Arg Glu Val Leu
 465 470 475 480

Glu Trp Arg Phe Asp Ser His Leu Ala Phe His His Val Ala Arg Glu
 485 490 495

Leu His Pro Glu Tyr Phe Lys Asn Cys
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<210> - 9

<211> 1689

<212> DNA

<213> Artificial sequence

<220>

<223> nucleotide sequence of RT insert of p7077-RT3

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 cctctggagc aggaacttttag aaagtacacc gcctttacca tcccatctat caacaacgag 420
 acccctggca tcagatatca gtacaacgtc ctccccagg gctggaagg gctctccgcc 480

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g t c a t c t a c c	a g t a c a t g g a	c g a c c t g t a c	g t g g g c t c t g	a c c t g g a a a t	c g g g c a g c a t	600
c g c a c g a a g a	t t g a g g a g c t	g a g g c a g c a t	c t g c t g a g a t	g g g g c c t g a c	c a c t c c g g a c	660
a a g a a g c a t c	a g a a g g a g c c	g c c a t t c c t g	t g g a t g g g c t	a c g a g c t c c a	t c c c g a c a a g	720
t g g a c c g t g c	a g c c t a t c g t	c c t c c c c g a g	a a g g a c a g c t	g g a c c g t g a a	c g a c a t c c a g	780
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g c c g a g c t c g	a g c t g g c t g a	g a a c c g g g a g	a t c c t g a a g g	a g c c c g t g c a	c g g c g t g t a c	960
t a t g a c c c c t	c c a a g g a c c t	g a t c g c c g a a	a t c c a g a a g c	a g g g c c a g g g	g c a g t g g a c a	1020
t a c c a g a t t t	a c c a g g a g c c	t t t c a a g a a c	c t c a a g a c c g	g c a a g t a c g c	c c g c a t g a g g	1080
g g c g c c c a c a	c c a a c g a t g t	c a a g c a g c t g	a c c g a g g c c g	t c c a g a a g a t	c a c g a c c g a g	1140
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g a g a c g t g g t	g g a c c g a a t a	t t g g c a g g c c	a c c t g g a t t c	c c g a g t g g g a	g t t c g t g a a t	1260
a c a c c t c c t c	t g g t g a a g c t	g t g g t a c c a g	c t c g a g a a g g	a g c c c a t c g t	g g g c g c g g a g	1320
a c a t t c t a c g	t g g a c g g c g c	g g c c a a c c g c	g a a a c a a a g c	t c g g g a a g g c	c g g g t a c g t c	1380
a c c a a c c g g g	g c c g c c a g a a	g g t c g t c a c c	c t g a c c g a c a	c c a c c a a c c a	g a a g a c g g a g	1440
c t g c a g g c c a	t c t a t c t c g c	t c t c c a g g a c	t c c g g c c t g g	a g g t g a a c a t	c g t g a c g g a c	1500
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c a t a a g g g c a	t t g g c g g c a a	c g a g c a g g t c	g a c a a g c t g g	t g a g t g c g g g	g a t t a g a a a g	1680
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<210> 10

<211> 562

<212> PRT

<213> Artificial sequence

<220>

<223> amino acid sequence of RT insert of p7077-RT3

<400> 10

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Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe Ala	50	55	60
Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe Arg	65	70	75
Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly Ile	85	90	95
Pro His Pro Ala Gly Leu Lys Lys Lys Lys Ser Val Thr Val Leu Asp	100	105	110
Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Glu Asp Phe Arg Lys	115	120	125
Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly Ile	130	135	140
Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro Ala	145	150	155
Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys Gln	165	170	175
Asn Pro Asp Ile Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val Gly	180	185	190
Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu Arg	195	200	205
Gln His Leu Leu Arg Trp Gly Leu Thr Thr Pro Asp Lys Lys His Gln	210	215	220
Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp Lys	225	230	235
Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr Val	245	250	255

Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln Ile
260 265 270

Tyr Pro Gly Ile Lys Val Arg Gln Leu Cys Lys Leu Leu Arg Gly Thr
275 280 285

Lys Ala Leu Thr Glu Val Ile Pro Leu Thr Glu Glu Ala Glu Leu Glu
290 295 300

Leu Ala Glu Asn Arg Glu Ile Leu Lys Glu Pro Val His Gly Val Tyr
305 310 315 320

Tyr Asp Pro Ser Lys Asp Leu Ile Ala Glu Ile Gln Lys Gln Gly Gln
325 330 335

Gly Gln Trp Thr Tyr Gln Ile Tyr Gln Glu Pro Phe Lys Asn Leu Lys
340 345 350

Thr Gly Lys Tyr Ala Arg Met Arg Gly Ala His Thr Asn Asp Val Lys
355 360 365

Gln Leu Thr Glu Ala Val Gln Lys Ile Thr Thr Glu Ser Ile Val Ile
370 375 380

Trp Gly Lys Thr Pro Lys Phe Lys Leu Pro Ile Gln Lys Glu Thr Trp
385 390 395 400

Glu Thr Trp Trp Thr Glu Tyr Trp Gln Ala Thr Trp Ile Pro Glu Trp
405 410 415

Glu Phe Val Asn Thr Pro Pro Leu Val Lys Leu Trp Tyr Gln Leu Glu
420 425 430

Lys Glu Pro Ile Val Gly Ala Glu Thr Phe Tyr Val Asp Gly Ala Ala
435 440 445

Asn Arg Glu Thr Lys Leu Gly Lys Ala Gly Tyr Val Thr Asn Arg Gly
450 455 460

Arg Gln Lys Val Val Thr Leu Thr Asp Thr Thr Asn Gln Lys Thr Glu
465 470 475 480

Leu Gln Ala Ile Tyr Leu Ala Leu Gln Asp Ser Gly Leu Glu Val Asn
485 490 495

Ile Val Thr Asp Ser Gln Tyr Ala Leu Gly Ile Ile Gln Ala Gln Pro
500 505 510

Asp Gln Ser Glu Ser Glu Leu Val Asn Gln Ile Ile Glu Gln Leu Ile
515 520 525

Lys Lys Glu Lys Val Tyr Leu Ala Trp Val Pro Ala His Lys Gly Ile
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Gly Gly Asn Glu Gln Val Asp Lys Leu Val Ser Ala Gly Ile Arg Lys
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Val Leu

<210> 11

<211> 1689

<212> DNA

<213> Artificial sequence

<220>

<223> nucleotide sequence of the coding insert in p73i-RT3

<400> 11

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cccgtgtttg ccatcaagaa gaaggacagc accaagtggc gcaagctggt ggatttccgg	240
gagctgaata agcggaccca ggatttctgg gaggtccagc tgggcatccc ccatccggcc	300
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cctctggacg aggactttag aaagtacacc gcctttacca tcccatctat caacaacgag	420
acctctggca tcagatatca gtacaacgtc ctccccagg gctggaaggg ctctcccgcc	480
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cgcacgaaga ttgaggagct gaggcagcat ctgctgagat ggggcctgac cactccggac	660
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tggaccgtgc agcctatcgt cctccccgag aaggacagct ggaccgtgaa cgacatccag	780

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aaccagatta tcgagcagct gatcaagaaa gagaaggctt acctcgctg ygtcccggcc 1620
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gtgctgtaa 1689

<210> 12

<211> 562

<212> PRT

<213> Artificial sequence

<220>

<223> amino acid sequence of the coding insert in p73i-RT3

<400> 12

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Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu Lys
20 25 30

Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly Lys
35 40 45

Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe Ala
 50 55 60

Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe Arg
 65 70 75 80

Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly Ile
 85 90 95

Pro His Pro Ala Gly Leu Lys Lys Lys Lys Ser Val Thr Val Leu Asp
 100 105 110

Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Glu Asp Phe Arg Lys
 115 120 125

Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly Ile
 130 135 140

Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro Ala
 145 150 155 160

Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys Gln
 165 170 175

Asn Pro Asp Ile Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val Gly
 180 185 190

Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu Arg
 195 200 205

Gln His Leu Leu Arg Trp Gly Leu Thr Thr Pro Asp Lys Lys His Gln
 210 215 220

Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp Lys
 225 230 235 240

Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr Val
 245 250 255

Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln Ile
 260 265 270

Tyr Pro Gly Ile Lys Val Arg Gln Leu Cys Lys Leu Leu Arg Gly Thr
 275 280 285

Lys Ala Leu Thr Glu Val Ile Pro Leu Thr Glu Glu Ala Glu Leu Glu
290 295 300

Leu Ala Glu Asn Arg Glu Ile Leu Lys Glu Pro Val His Gly Val Tyr
305 310 315 320

Tyr Asp Pro Ser Lys Asp Leu Ile Ala Glu Ile Gln Lys Gln Gly Gln
325 330 335

Gly Gln Trp Thr Tyr Gln Ile Tyr Gln Glu Pro Phe Lys Asn Leu Lys
340 345 350

Thr Gly Lys Tyr Ala Arg Met Arg Gly Ala His Thr Asn Asp Val Lys
355 360 365

Gln Leu Thr Glu Ala Val Gln Lys Ile Thr Thr Glu Ser Ile Val Ile
370 375 380

Trp Gly Lys Thr Pro Lys Phe Lys Leu Pro Ile Gln Lys Glu Thr Trp
385 390 395 400

Glu Thr Trp Trp Thr Glu Tyr Trp Gln Ala Thr Trp Ile Pro Glu Trp
405 410 415

Glu Phe Val Asn Thr Pro Pro Leu Val Lys Leu Trp Tyr Gln Leu Glu
420 425 430

Lys Glu Pro Ile Val Gly Ala Glu Thr Phe Tyr Val Asp Gly Ala Ala
435 440 445

Asn Arg Glu Thr Lys Leu Gly Lys Ala Gly Tyr Val Thr Asn Arg Gly
450 455 460

Arg Gln Lys Val Val Thr Leu Thr Asp Thr Thr Asn Gln Lys Thr Glu
465 470 475 480

Leu Gln Ala Ile Tyr Leu Ala Leu Gln Asp Ser Gly Leu Glu Val Asn
485 490 495

Ile Val Thr Asp Ser Gln Tyr Ala Leu Gly Ile Ile Gln Ala Gln Pro
500 505 510

Asp Gln Ser Glu Ser Glu Leu Val Asn Gln Ile Ile Glu Gln Leu Ile
515 520 525

Lys Lys Glu Lys Val Tyr Leu Ala Trp Val Pro Ala His Lys Gly Ile
530 535 540

Gly Gly Asn Glu Gln Val Asp Lys Leu Val Ser Ala Gly Ile Arg Lys
545 550 555 560

Val Leu